

The opinion in support of the decision being entered today was not written for publication and is not binding precedent of the Board.

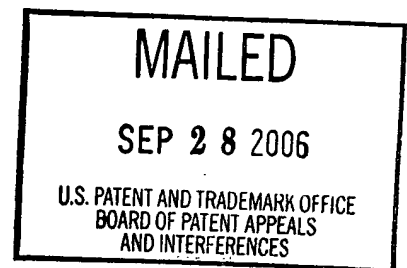
UNITED STATES PATENT AND TRADEMARK OFFICE

**BEFORE THE BOARD OF PATENT APPEALS
AND INTERFERENCES**

Ex parte RICHARD J. FELDMANN

Appeal No. 2006-2194
Application No. 09/866,925

ON BRIEF



Before ADAMS, GREEN, and LEOVITZ, Administrative Patent Judges.

GREEN, Administrative Patent Judge.

VACATUR AND REMAND TO THE EXAMINER

On consideration of the record, we find that this case is not susceptible to meaningful review and is thus not in condition for a decision on appeal.

Accordingly, we vacate the pending rejections and remand the application to the examiner to consider the issues discussed herein and take appropriate action not inconsistent with the views expressed herein. Lest there be any

misunderstanding, the term "vacate" in this context means to set aside or void.

When the Board vacates an examiner's rejection, the rejection is set aside and

no longer exists. Cf. Ex parte Zambrano, 58 USPQ2d 1312, 1313 (Bd. Pat. App. & Int. 2001).

BACKGROUND

According to the specification:

This patent application shows how two specific adjacent RNA single-stranded sequences (called C1 and C2 – for Control Sequence 1 and Control Sequence 2) interact with two distant double-stranded DNA sequences (called T1 and T2 – for Target Sequence 1 and Target Sequence 2) to form a tetradic relationship which is called a “connectron.” The two distant DNA double-stranded sequences (T1 and T2) must be on the same chromosome in a genome and they must be between 1kb and 105kb of each other. The adjacent single-stranded RNA sequences (C1/C2) can be on the same or different chromosomes as the T1 and T2 sequences. The C1 sequence is identical to the T1 sequence and the C2 sequence is identical to the T2 sequence. The connectron acts to stabilize the double-stranded DNA by allowing 30nm chromatin particles to form. Genes that lie between T1 and T2 sequences when wrapped up in 30 nm chromatin particles are not open to promotion and expression.

Id. at 1-2.

Moreover,

[c]haracteristically the adjacent C1/C2 sequences lie in the 3'UTR of a gene. The T1 and T2 sequences do not lie within the translated region of any gene. These sequences “surround” one or more genes.

Id. at 2.

A “possible connectron” is defined by the specification as:

Any set of T1, T2 and C1/C2 sequences such that the C1 sequence is identical to the T1 sequence and the C2 sequence is identical to the T2 sequence. The promoter of some gene causes the mRNA of the gene to be expressed. The mRNA is edited to eliminate the introns. The whole mRNA including the 3'UTR can move about in the cell or the nucleus of the cell. The C1/C2 RNA that is part of the 3'UTR moves to the T1 and T2 DNA sequences.

A triple-stranded complex of the DNA and RNA forms such that the C1 sequence forms hydrogen bonds with the T1 sequence and the C2 sequence forms hydrogen bonds with the T2 sequence. Because the C1 sequence is adjacent to the C2 sequence, the T1 sequence is brought physically close to the T2 sequence. This produces a loop of between 1kb and 150kb in the DNA. Histone proteins reduce the length of the DNA by binding 200 bases. Histone/DNA complexes form six-fold symmetry chromatin assemblies. The diameter of the chromatin assemblies is approximately 30nm.

Id. at 6-7.

The specification states that an algorithm has been developed “to determine the connectron structure of any genome,” id. at 2, and Figure 8 provides an overall view of the algorithm, see id. at 25. The “connectron invention” “depends only on sequence equivalency.” Id. at 28. As can be seen in Figure 8, the algorithm analyzes a genome for possible connectrons. Moreover, according to the specification, the physical experimentation process of proving the existence and lifetimes of connectrons “is logically quite separate from the computational experimentation that have been conducted from June of 1999 to May of 2001,” id. at 28, which has demonstrated the existence of connectrons in prokaryotes, plants, higher animals and humans using publicly available genomes, see id. at 35, 37 and 38.

Claim 20, which is only one of the eight independent claims, is drawn to:

A computer mediated method of identifying DNA sequences that control the expression of different collections of genes in a genome comprising detecting, by computer, one or more pairs of first and second non-adjacent DNA sequences which could bind to one RNA molecule such that a first RNA sequence in that RNA molecule can bind a first non-adjacent DNA sequence and a second RNA sequence in that RNA molecule can bind to a second non-adjacent sequence.

VACATUR AND REMAND

The board serves as a board of review, not a de novo examination tribunal. See 35 U.S.C. § 6(b) (“The [board] shall, on written appeal of an applicant, review adverse decisions of examiners upon applications for patents.”). The burden is on the examiner to set forth a prima facie case of nonpatentability. See In re Alton, 76 F.3d 1168, 1175, 37 USPQ2d 1578, 1581 (Fed. Cir. 1996).

Claims 20-37, all of the claims on appeal, stand rejected under 35 U.S.C. § 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The rejection is set forth on pages 3-5 of the Examiner’s Answer, but it suffers from several deficiencies.

First, there are eight independent claims, each having different limitations. For example, claim 21 requires “detecting, by computer, changes in connectron behavior in the genome as a function of changes in the sequence of the genome.” The rejection, however, does not address the limitations of all of the independent claims, nor does it address the limitations of dependent claims 37.

Second, the rejection appears to address limitations that do not seem to appear in the claims. The examiner focuses on the issue that “[i]n order to practice the claimed invention one of skill in the art must identify and use a connectron to predict regulation of gene expression.” Examiner’s Answer, page

3. Claim 20, for example, does not require predicting regulation of gene expression, but only appears to require locating possible connectrons.

Last, and most importantly, neither the examiner nor appellant appears to have engaged in any sort of claim construction, nor have they appeared to have reached a “meeting of the minds” on how the claims should be interpreted. As set forth in In re Zletz, 893 F.2d 319, 321-22, 13 USPQ2d 1320, 1322 (Fed. Cir. 1989):

[D]uring patent prosecution when claims can be amended, ambiguities should be recognized, scope and breadth of language explored, and clarification imposed. . . . An essential purpose of patent examination is to fashion claims that are precise, clear, correct, and unambiguous. Only in this way can uncertainties of claim scope be removed, as much as possible, during the administrative process.

Moreover, we remind the examiner and appellant that analyzing claims based on “speculation as to meaning of the terms employed and assumptions as to the scope of such claims” is legal error. In re Steele, 305 F.2d 859, 862, 134 USPQ 292, 295 (CCPA 1962).

Thus, upon return of the application, the examiner should engage in the claim construction analysis, and address any issues that may arise based on that analysis. For the convenience of the examiner and appellant, we have provided some examples of such issues, but this should not be seen as an exhaustive of all such issues that may exist.

Claim 20 appears to be drawn to a method of detecting pairs of non-adjacent DNA sequences which can bind to two regions of an RNA molecule. As such, the claim is very broad, and is not limited to identifying “connectrons.”

Francois¹ teaches that “oligonucleotides consisting of two oligomer sequences linked by a chemical tether can also bind two single-stranded noncontiguous sites in RNA with secondary structures.” Id. at page 65, column 2. Thus, it would have been obvious to thus use a computer design the oligonucleotide consisting of two oligomer sequences (reads on a pair of non-adjacent DNA sequences” and then predict its binding to the noncontiguous sites of the RNA (reads on two regions of an RNA molecule), which appears to be all that is required by claim 20.

Claim 22 recites “detecting [by computer] changes in expression of different gene collections in a genome that result in the level of control sequences caused by exogenous stimuli.” At first blush, this claim appears to have many issues.

One issue appears to be that the claim is indefinite under 35 U.S.C. § 112, second paragraph. It is unclear if the exogenous stimuli is physical or computational. If it is physical, it is unclear how that step is being performed in the context of the computational method.

If the exogenous stimuli is computational, the claim would not appear to meet the written description and/or enablement requirements of 35 U.S.C. § 112, first paragraph.² As discussed in the background, the specification teaches a

¹ Francois et al. (Francois), Recognition and Cleavage of Single-Stranded DNA Containing Hairpin Structures by Oligonucleotides Forming Both Watson-Crick and Hoogsteen Hydrogen Bonds,” Biochemistry, Vol. 34, pp. 65-72 (1995), first page only.

² We recognize that the written description and enablement requirements of 35 U.S.C. § 112, first paragraph, are distinct, and should be analyzed separately. See Vas-Cath Inc. v. Mahurkar, 935 F.2d 1555, 1563-64, 19 USPQ2d 1111, 1116-17 (Fed. Cir. 1991) (noting that the requirement for written description under the first paragraph of section 112 is separate and distinct from the

computational method of identifying possible connectrons, which is entirely separate from the physical experimentation process. First, the specification does not appear to describe a process of computationally adding exogenous stimuli and then looking at the level of connectron control. Second, such a claim would not appear to be enabled as the specification does not teach an algorithm which could perform such a calculation, nor does it teach what type of stimuli may be applied, or the correlation between any such stimuli and connectron control.

We note that similar issues appear to exist for each of the remaining independent claims.

Claims 28-37 all depend from claim 20, and state “[u]sing the method as defined in claim 20.” A “use” or “using” claim, however, is not statutory subject matter, and the claims should be rejected under 35 U.S.C. § 101. See MPEP 2173.05(q). In addition, the examiner may wish to also explore a rejection under 35 U.S.C. § 112, second paragraph, as it is unclear what method steps are being added by these dependent claims to the method set forth in claim 20.

Again, these examples are not exhaustive, and the examiner should undertake a more thorough analysis of all the claims as to whether they meet the statutory requirements of § 101, § 102, § 103 and § 112.

FUTURE PROCEEDINGS

The case is being returned to the jurisdiction of the examiner for further action not inconsistent with this opinion.

enablement requirement of that paragraph). We only discuss them together here for the sake of expediency.

If prosecution is resumed, we state that we are not authorizing a
Supplemental Examiner's Answer.

VACATED and REMANDED



Donald E. Adams
Administrative Patent Judge

Lora M. Green
Administrative Patent Judge



Richard M. Lebovitz
Administrative Patent Judge

)
)
)
) BOARD OF PATENT
) APPEALS AND
) INTERFERENCES
)

Appeal No. 2006-2194
Application No. 09/866,925

Page 9

Law Office of Jim Zegeer
801 North Pitt Street, #108
Alexandria VA 22314